

<110> Merck & Co., Inc.

<130> 21471 PCT

<151> 2004-01-09

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<170> FastSEQ for Windows Version 4.0
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<211> 571

<213> Artificial Sequence

<223> modified HCV NS5B

1/16

Tyr Arg Ala Cys Ser Leu Pro Glu Glu Ala His Thr Ala Ile His Ser
 245 250 255
 Leu Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly
 260 265 270
 Gln Thr Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr
 275 280 285
 Ser Met Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys
 290 295 300
 Lys Ala Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp
 305 310 315 320
 Leu Val Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn
 325 330 335
 Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
 340 345 350
 Asp Pro Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
 355 360 365
 Ser Asn Val Ser Val Ala Leu Gly Pro Gln Gly Arg Arg Arg Tyr Tyr
 370 375 380
 Leu Thr Arg Asp Pro Thr Thr Pro Ile Ala Arg Ala Ala Trp Glu Thr
 385 390 395 400
 Val Arg His Ser Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Gln Tyr
 405 410 415
 Ala Pro Thr Ile Trp Ala Arg Met Val Leu Met Thr His Phe Phe Ser
 420 425 430
 Ile Leu Met Ala Gln Asp Thr Leu Asp Gln Asn Leu Asn Phe Glu Met
 435 440 445
 Tyr Gly Ala Val Tyr Ser Val Ser Pro Leu Asp Leu Pro Ala Ile Ile
 450 455 460
 Glu Arg Leu His Gly Leu Asp Ala Phe Ser Leu His Thr Tyr Thr Pro
 465 470 475 480
 His Glu Leu Thr Arg Val Ala Ser Ala Leu Arg Lys Leu Gly Ala Pro
 485 490 495
 Pro Leu Arg Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu
 500 505 510
 Ile Ser Arg Gly Gly Arg Ala Ala Val Cys Gly Arg Tyr Leu Phe Asn
 515 520 525
 Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Arg
 530 535 540
 Leu Leu Asp Leu Ser Ser Trp Phe Thr Val Gly Ala Gly Gly Gly Asp
 545 550 555 560
 Ile Tyr His Ser Val Ser Arg Ala Arg Pro Arg
 565 570

<210> 2

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> modified HCV NS5B

<400> 2

Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Gly
 1 5 10 15

Pro	Glu	Glu	Glu	Lys	Leu	Pro	Ile	Asn	Pro	Leu	Ser	Asn	Ser	Leu	Met	20	25	30
Arg	Phe	His	Asn	Lys	Val	Tyr	Ser	Thr	Thr	Ser	Arg	Ser	Ala	Ser	Leu	35	40	45
Arg	Ala	Lys	Lys	Val	Thr	Phe	Asp	Arg	Val	Gln	Val	Leu	Asp	Ala	His	50	55	60
Tyr	Asp	Ser	Val	Leu	Gln	Asp	Val	Lys	Arg	Ala	Ala	Ser	Lys	Val	Ser	65	70	75
Ala	Arg	Leu	Leu	Thr	Val	Glu	Glu	Ala	Cys	Ala	Leu	Thr	Pro	Pro	His	85	90	95
Ser	Ala	Lys	Ser	Arg	Tyr	Gly	Phe	Gly	Ala	Lys	Glu	Val	Arg	Ser	Leu	100	105	110
Ser	Arg	Arg	Ala	Val	Asn	His	Ile	Arg	Ser	Val	Trp	Glu	Asp	Leu	Leu	115	120	125
Glu	Asp	Gln	His	Thr	Pro	Ile	Asp	Thr	Thr	Ile	Met	Ala	Lys	Asn	Glu	130	135	140
Val	Phe	Cys	Ile	Asp	Pro	Thr	Lys	Gly	Gly	Lys	Lys	Pro	Ala	Arg	Leu	145	150	155
Ile	Val	Tyr	Pro	Asp	Leu	Gly	Val	Arg	Val	Cys	Glu	Lys	Met	Ala	Leu	165	170	175
Tyr	Asp	Ile	Ala	Gln	Lys	Leu	Pro	Lys	Ala	Ile	Met	Gly	Pro	Ser	Tyr	180	185	190
Gly	Phe	Gln	Tyr	Ser	Pro	Ala	Glu	Arg	Val	Asp	Phe	Leu	Leu	Lys	Ala	195	200	205
Trp	Gly	Ser	Lys	Lys	Asp	Pro	Met	Gly	Phe	Ser	Tyr	Asp	Thr	Arg	Cys	210	215	220
Phe	Asp	Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Thr	Glu	Glu	Ser	Ile	225	230	235
Tyr	Gln	Ala	Cys	Ser	Leu	Pro	Gln	Glu	Ala	Arg	Thr	Val	Ile	His	Ser	245	250	255
Leu	Thr	Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Thr	Asn	Ser	Lys	Gly	260	265	270
Gln	Ser	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Phe	Thr	Thr	275	280	285
Ser	Met	Gly	Asn	Thr	Met	Thr	Cys	Tyr	Ile	Lys	Ala	Leu	Ala	Ala	Cys	290	295	300
Lys	Ala	Ala	Gly	Ile	Val	Asp	Pro	Val	Met	Leu	Val	Cys	Gly	Asp	Asp	305	310	315
Leu	Val	Val	Ile	Ser	Glu	Ser	Gln	Gly	Asn	Glu	Glu	Asp	Glu	Arg	Asn	325	330	335
Leu	Arg	Ala	Phe	Thr	Glu	Ala	Met	Thr	Arg	Tyr	Ser	Ala	Pro	Pro	Gly	340	345	350
Asp	Leu	Pro	Arg	Pro	Glu	Tyr	Asp	Leu	Glu	Leu	Ile	Thr	Ser	Cys	Ser	355	360	365
Ser	Asn	Val	Ser	Val	Ala	Leu	Asp	Ser	Arg	Gly	Arg	Arg	Arg	Tyr	Phe	370	375	380
Leu	Thr	Arg	Asp	Pro	Thr	Thr	Pro	Ile	Thr	Arg	Ala	Ala	Trp	Glu	Thr	385	390	395
Val	Arg	His	Ser	Pro	Val	Asn	Ser	Trp	Leu	Gly	Asn	Ile	Ile	Gln	Tyr	405	410	415
Ala	Pro	Thr	Ile	Trp	Val	Arg	Met	Val	Ile	Met	Thr	His	Phe	Phe	Ser	420	425	430
Ile	Leu	Leu	Ala	Gln	Asp	Thr	Leu	Asn	Gln	Asn	Leu	Asn	Phe	Glu	Met	435	440	445

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Tyr Gly Ala Val Tyr Ser Val Asn Pro Leu Asp Leu Pro Ala Ile Ile
  450          455          460
Glu Arg Leu His Gly Leu Glu Ala Phe Ser Leu His Thr Tyr Ser Pro
465          470          475          480
His Glu Leu Ser Arg Val Ala Ala Thr Leu Arg Lys Leu Gly Ala Pro
          485          490          495
Pro Leu Arg Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu
          500          505          510
Ile Ala Gln Gly Ala Arg Ala Ala Ile Cys Gly Arg Tyr Leu Phe Asn
          515          520          525
Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Ser
          530          535          540
Arg Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Gly Asp
545          550          555          560
Ile Tyr His Ser Val Ser His Ala Arg Pro Arg
          565          570

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<210> 3
 <211> 571
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> modified HCV NS5B

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<400> 3
Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ser
  1          5          10          15
Ala Glu Glu Glu Lys Leu Pro Ile Ser Pro Leu Ser Asn Ser Leu Leu
          20          25          30
Arg His His Asn Leu Val Tyr Ser Thr Ser Ser Arg Ser Ala Ser Gln
          35          40          45
Arg Gln Arg Lys Val Thr Phe Asp Arg Leu Gln Val Leu Asp Asp His
          50          55          60
Tyr Lys Thr Ala Leu Lys Glu Val Lys Glu Arg Ala Ser Arg Val Lys
65          70          75          80
Ala Arg Met Leu Thr Ile Glu Glu Ala Cys Ala Leu Val Pro Pro His
          85          90          95
Ser Ala Arg Ser Lys Phe Gly Tyr Ser Ala Lys Asp Val Arg Ser Leu
          100          105          110
Ser Ser Arg Ala Ile Asp Gln Ile Arg Ser Val Trp Glu Asp Leu Leu
          115          120          125
Glu Asp Thr Thr Thr Pro Ile Pro Thr Thr Ile Met Ala Lys Asn Glu
          130          135          140
Val Phe Cys Val Asp Pro Ala Lys Gly Gly Arg Lys Pro Ala Arg Leu
145          150          155          160
Ile Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Arg Ala Leu
          165          170          175
Tyr Asp Val Ile Gln Lys Leu Ser Ile Glu Thr Met Gly Ser Ala Tyr
          180          185          190
Gly Phe Gln Tyr Ser Pro Gln Gln Arg Val Glu Arg Leu Leu Lys Met
          195          200          205
Trp Thr Ser Lys Lys Thr Pro Leu Gly Phe Ser Tyr Asp Thr Arg Cys
210          215          220

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Phe Asp Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile
225                230                235                240
Tyr Gln Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser
                245                250                255
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
                260                265                270
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
                275                280                285
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
290                295                300
Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp
305                310                315                320
Leu Val Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala
                325                330                335
Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
                340                345                350
Asp Ala Pro Gln Pro Thr Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
                355                360                365
Ser Asn Val Ser Val Ala Arg Asp Asp Lys Gly Arg Arg Tyr Tyr Tyr
370                375                380
Leu Thr Arg Asp Ala Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr
385                390                395                400
Ala Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Tyr
                405                410                415
Ala Pro Thr Ile Trp Val Arg Met Val Met Met Thr His Phe Phe Ser
                420                425                430
Ile Leu Gln Ser Gln Glu Ile Leu Asp Arg Pro Leu Asp Phe Glu Met
                435                440                445
Tyr Gly Ala Thr Tyr Ser Val Thr Pro Leu Asp Leu Pro Ala Ile Ile
450                455                460
Glu Arg Leu His Gly Leu Ser Ala Phe Thr Leu His Ser Tyr Ser Pro
465                470                475                480
Val Glu Leu Asn Arg Val Ala Gly Thr Leu Arg Lys Leu Gly Cys Pro
                485                490                495
Pro Leu Arg Ala Trp Arg His Arg Ala Arg Ala Val Arg Ala Lys Leu
500                505                510
Ile Ala Gln Gly Gly Lys Ala Lys Ile Cys Gly Leu Tyr Leu Phe Asn
515                520                525
Trp Ala Val Arg Thr Lys Thr Asn Leu Thr Pro Leu Pro Ala Thr Gly
530                535                540
Gln Leu Asp Leu Ser Ser Trp Phe Thr Val Gly Val Gly Gly Asn Asp
545                550                555                560
Ile Tyr His Ser Val Ser Arg Ala Arg Thr Arg
                565                570

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<210> 4

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> modified HCV NS5B

<400> 4

Met	Ser	Met	Ser	Tyr	Thr	Trp	Thr	Gly	Ala	Leu	Val	Thr	Pro	Cys	Ala
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Ala	Glu	Glu	Ser	Lys	Leu	Pro	Ile	Ser	Pro	Leu	Ser	Asn	Ser	Leu	Leu
			20					25					30		
Arg	His	His	Asn	Met	Val	Tyr	Ala	Thr	Thr	Thr	Arg	Ser	Ala	Val	Thr
			35				40					45			
Arg	Gln	Lys	Lys	Val	Thr	Phe	Asp	Arg	Leu	Gln	Val	Val	Asp	Ser	His
			50			55					60				
Tyr	Asn	Glu	Val	Leu	Lys	Glu	Ile	Lys	Ala	Arg	Ala	Ser	Arg	Val	Lys
65					70					75					80
Ala	Arg	Leu	Leu	Thr	Thr	Glu	Glu	Ala	Cys	Asp	Leu	Thr	Pro	Pro	His
				85					90					95	
Ser	Ala	Arg	Ser	Lys	Phe	Gly	Tyr	Gly	Ala	Lys	Asp	Val	Arg	Ser	His
			100					105						110	
Ser	Arg	Lys	Ala	Ile	Asn	His	Ile	Ser	Ser	Val	Trp	Lys	Asp	Leu	Leu
			115				120					125			
Asp	Asp	Asn	Asn	Thr	Pro	Ile	Pro	Thr	Thr	Ile	Met	Ala	Lys	Asn	Glu
			130			135					140				
Val	Phe	Ala	Val	Asn	Pro	Ala	Lys	Gly	Gly	Arg	Lys	Pro	Ala	Arg	Leu
145					150					155					160
Ile	Val	Tyr	Pro	Asp	Leu	Gly	Val	Arg	Val	Cys	Glu	Lys	Arg	Ala	Leu
				165					170					175	
His	Asp	Val	Ile	Lys	Lys	Leu	Pro	Glu	Ala	Val	Met	Gly	Ala	Ala	Tyr
			180					185					190		
Gly	Phe	Gln	Tyr	Ser	Pro	Ala	Gln	Arg	Val	Glu	Phe	Leu	Leu	Thr	Ala
			195				200					205			
Trp	Lys	Ser	Lys	Lys	Thr	Pro	Met	Gly	Phe	Ser	Tyr	Asp	Thr	Arg	Cys
			210			215					220				
Phe	Asp	Ser	Thr	Val	Thr	Glu	Lys	Asp	Ile	Arg	Val	Glu	Glu	Glu	Val
225					230					235					240
Tyr	Gln	Cys	Cys	Asp	Leu	Glu	Pro	Glu	Ala	Arg	Lys	Val	Ile	Thr	Ala
				245					250					255	
Leu	Thr	Asp	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	His	Asn	Ser	Lys	Gly
				260				265					270		
Asp	Leu	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Tyr	Thr	Thr
			275				280					285			
Ser	Phe	Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Thr	Ala	Ala	Ile
			290				295				300				
Arg	Ala	Ala	Gly	Leu	Arg	Asp	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp
305					310					315					320
Leu	Val	Val	Ile	Ala	Glu	Ser	Asp	Gly	Val	Glu	Glu	Asp	Asn	Arg	Ala
				325					330					335	
Leu	Arg	Ala	Phe	Thr	Glu	Ala	Met	Thr	Arg	Tyr	Ser	Ala	Pro	Pro	Gly
			340					345					350		
Asp	Ala	Pro	Gln	Pro	Ala	Tyr	Asp	Leu	Glu	Leu	Ile	Thr	Ser	Cys	Ser
			355				360					365			
Ser	Asn	Val	Ser	Val	Ala	His	Asp	Val	Thr	Gly	Lys	Lys	Val	Tyr	Tyr
			370				375				380				
Leu	Thr	Arg	Asp	Pro	Glu	Thr	Pro	Leu	Ala	Arg	Ala	Ala	Trp	Glu	Thr
385					390					395					400
Val	Arg	His	Thr	Pro	Val	Asn	Ser	Trp	Leu	Gly	Asn	Ile	Ile	Val	Tyr
				405					410					415	
Ala	Pro	Thr	Ile	Trp	Val	Arg	Met	Ile	Leu	Met	Thr	His	Phe	Phe	Ser
			420					425					430		

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Ile Leu Gln Ser Gln Glu Ala Leu Glu Lys Ala Leu Asp Phe Asp Met
      435      440      445
Tyr Gly Val Thr Tyr Ser Ile Thr Pro Leu Asp Leu Pro Ala Ile Ile
      450      455      460
Gln Arg Leu His Gly Leu Ser Ala Phe Thr Leu His Gly Tyr Ser Pro
465      470      475      480
His Glu Leu Asn Arg Val Ala Gly Ala Leu Arg Lys Leu Gly Val Pro
      485      490      495
Pro Leu Arg Ala Trp Arg His Arg Ala Arg Ala Val Arg Ala Lys Leu
      500      505      510
Ile Ala Gln Gly Gly Arg Ala Lys Ile Cys Gly Ile Tyr Leu Phe Asn
      515      520      525
Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Ala Ala Ala
      530      535      540
Lys Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Gly Asp
545      550      555      560
Ile Tyr His Ser Met Ser His Ala Arg Pro Arg
      565      570

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<210> 5
<211> 571
<212> PRT
<213> Artificial Sequence

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<220>
<223> modified HCV NS5B

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<400> 5
Met Ser Met Ser Tyr Thr Trp Thr Gly Ala Leu Ile Thr Pro Cys Ala
1      5      10      15
Ala Glu Glu Glu Lys Leu Pro Ile Asn Pro Leu Ser Asn Ser Leu Ile
      20      25      30
Arg His His Asn Met Val Tyr Ser Thr Thr Ser Arg Ser Ala Ser Leu
      35      40      45
Arg Gln Lys Lys Val Thr Phe Asp Arg Val Gln Val Phe Asp Gln His
      50      55      60
Tyr Gln Glu Ile Leu Lys Glu Ile Lys Leu Arg Ala Ser Lys Val Gln
65      70      75      80
Ala Lys Leu Leu Ser Val Glu Glu Ala Cys Asp Leu Thr Pro Ser His
      85      90      95
Ser Ala Arg Ser Lys Tyr Gly Tyr Gly Ala Gln Asp Val Arg Ser His
      100     105     110
Ala Ser Lys Ala Val Asn His Ile Arg Ser Val Trp Glu Asp Leu Leu
      115     120     125
Glu Asp Ser Asp Thr Pro Ile Pro Thr Thr Ile Met Ala Lys Asn Glu
      130     135     140
Val Phe Cys Val Asp Pro Ser Lys Gly Gly Arg Lys Pro Ala Arg Leu
145     150     155     160
Ile Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu
      165     170     175
Tyr Asp Val Thr Gln Lys Leu Pro Gln Ala Val Met Gly Ser Ala Tyr
      180     185     190
Gly Phe Gln Tyr Ser Pro Thr Gln Arg Val Glu Tyr Leu Leu Lys Met
      195     200     205

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Trp Arg Ser Lys Lys Val Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys
 210                215                220
Phe Asp Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Asn Asp Ile
225                230                235                240
Tyr Gln Ser Cys Gln Leu Asp Pro Val Ala Arg Arg Ala Val Ser Ser
                245                250                255
Leu Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Val Asn Ser Lys Gly
                260                265                270
Gln Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
                275                280                285
Ser Met Gly Asn Thr Ile Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys
                290                295                300
Arg Ala Ala Asn Ile Lys Asp Cys Asp Met Leu Val Cys Gly Asp Asp
305                310                315                320
Leu Val Val Ile Cys Glu Ser Ala Gly Val Gln Glu Asp Thr Glu Ser
                325                330                335
Leu Arg Ala Phe Thr Asp Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly
                340                345                350
Asp Ala Pro Gln Pro Thr Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser
                355                360                365
Ser Asn Val Ser Val Ala His Asp Gly Asn Gly Lys Arg Tyr Tyr Tyr
                370                375                380
Leu Thr Arg Asp Cys Thr Thr Pro Leu Ala Arg Ala Ala Trp Glu Thr
385                390                395                400
Ala Arg His Thr Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Met Phe
                405                410                415
Ala Pro Thr Ile Trp Val Arg Met Val Leu Met Thr His Phe Phe Ser
                420                425                430
Ile Leu Gln Ser Gln Glu Gln Leu Glu Lys Ala Leu Asp Phe Asp Ile
                435                440                445
Tyr Gly Val Thr Tyr Ser Val Ser Pro Leu Asp Leu Pro Ala Ile Ile
                450                455                460
Gln Arg Leu His Gly Met Ala Ala Phe Ser Leu His Gly Tyr Ser Pro
465                470                475                480
Val Glu Leu Asn Arg Val Gly Ala Cys Leu Arg Lys Leu Gly Val Pro
                485                490                495
Pro Leu Arg Ala Trp Arg His Arg Ala Arg Ala Val Arg Ala Lys Leu
                500                505                510
Ile Ala Gln Gly Gly Lys Ala Ala Ile Cys Gly Lys Tyr Leu Phe Asn
                515                520                525
Trp Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Val Ser Ala Ser
                530                535                540
Lys Leu Asp Leu Ser Gly Trp Phe Val Ala Gly Tyr Asp Gly Gly Asp
545                550                555                560
Ile Tyr His Ser Val Ser Gln Ala Arg Pro Arg
                565                570

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<210> 6

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding SEQ ID NO: 1

<400> 6

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accacaacaa agagcgctc actaagggtc aaaaaggtaa cttttgatag gatgcaagtg 180
ctcgactcct actacgactc agtcttaaag gacattaagc tagcggcctc caaggtcacc 240
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aagtccgtgt ggaaggacct cctggaggac tcagaaacac caattccac aaccattatg 420
gccaaaaatg aggtgttctg cgtggacccc accaaggggg gcaagaaagc agctcgcctt 480
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gatacccgat gctttgactc aaccgtcact gagagagaca tcaggactga ggagtccata 720
tatcgggcct gctccttgcc cgaggaggcc cacttgcca tacactcgt aactgagaga 780
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cgggaggcgc gcctcctgga tttatccagc tggttcaccg tcggcgcccg cgggggcgac 1680
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<210> 7

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding SEQ ID NO: 2

<400> 7

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acaacctcaa ggagtgcctc tctgagggca aagaagggtga cttttgacag ggtgcagggtg 180
ctggacgcac actatgactc agtcttgacg gacgttaagc gggccgcctc taaggttagt 240
gcgaggctcc tcacggtaga ggaagcctgc gcgctgacct cggccctactc cgccaaatcg 300
cgatacggat ttggggcaca agagggtgag agcttatcca ggaggggcgt taaccacatc 360
cggctccgtgt gggaggacct cctggaagac caacataccc caattgacac aactatcatg 420
gctaaaaatg aggtgttctg cattgatcca actaaagggt ggaaaaagcc agctcgcctc 480
atcgataacc ccgaccttgg ggtcagggtg tgcgaaaaga tggccctcta tgacatcgca 540
caaaagcttc ccaaagcgat aatggggcca tcctatgggt tccaataact tcccgcagaa 600
cgggtcgatt tcctcctcaa agcttgggga agtaagaagg acccaatggg gttctcgtat 660
gacaccgctt gctttgactc aaccgtcacg gagagggaca taagaacaga agaatccata 720
tatcaggctt gttctctgcc tcaagaagcc agaactgtca tacactcgt cactgagaga 780
ctttacgtag gagggcccat gacaaacagc aaagggcaat cctgcggcta caggcgttgc 840
cgcgcaagcg gtgttttcac caccagcatg gggaatacca tgacatgtta catcaaagcc 900

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cccgaggcga gccgcctgga tttatccggg tggttcaccg tgggcgcggg cgggggcgac 1680
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<210> 8

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding SEQ ID NO: 3

<400> 8

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acgtcgtcga gaagcgcttc ccagcgtcag aggaagggtta ccttcgacag actgcagggtg 180
ctcgacgacc attataagac tgcattaaag gaggtgaagg agcgagcgtc taggggtgaag 240
gccgcactgc tcaccatcga ggaagcgtgc gcgtcgtcc ctctcactc tgcccggctc 300
aagttcgggt atagtgcgaa ggacgttcgc tccttggtcca gcagggccat tgaccagatc 360
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gcgaagaacg aggtgttttg tgtggacccc gctaaagggg gccgcaagcc cgctcgcttc 480
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cgggtcgaac gtctactgaa gatgtggacc tcaaagaaaa cccccttggg gttctcatat 660
gacaccgctt gctttgactc aactgtcact gaacaggaca tcagggtaga agaggagata 720
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ccagccactg gccagttgga cttgtccagc tggtttacgg ttggtgtcgg cgggaacgac 1680
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<210> 9

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding SEQ ID NO: 4

<400> 9

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gcacgcttgc ttaccacaga ggaagcttgc gacctgacgc cccccactc agccagatca 300
aagttcggct acggggcgaa ggatgttcgg agccattccc gcaaggccat taaccacatc 360
agctccgtgt ggaaggactt gctggacgac aacaataccc caataccaac aacaatcatg 420
gccaaaaatg aggtcttcgc tgtgaaccca gcgaaggag gtcggaagcc tgctcgcctg 480
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aaaaaactgc ctgaggccgt gatgggagcc gcttatggct tccaatactc cccagcgcag 600
cgggtggaat ttcttctgac tgcttggag tcgaagaaga cccaatggg gttctcttat 660
gatacccgct gctttgactc cactgtaacc gaaaaggaca tcagggtcga ggaagaggtc 720
tatcagtgtt gtgacctgga gccgaagcc cgcaaagtca tcaccgccct cacagataga 780
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atztatcaca gcatgtctca tgcccagacc cgc 1713

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<210> 10

<211> 1713

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotide sequence encoding SEQ ID NO: 5

<400> 10

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accacatcac gcagcgccag cctccgccag aagaagggtca catttgacag agtgcaagtg 180
ttcgaccaac attaccagga aatactaaag gagattaagc ttcgagcgtc caaggtgcag 240
gcgaagctct tatccgtaga ggaagcctgc gacctcacac catcgcactc agcccgggtc 300
aaatatgggt atggtgcaca ggacgttaga agccatgcta gcaaggccgt caaccacatc 360
cgctccgtgt gggaggactt gctagaagac tctgatactc caattcccac aaccatcatg 420
gctaagaatg aagtcttctg cgtagatccg tcgaagggtg gacgcaagcc ggcacgctta 480

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atagtgttacc cagacttggg cgtgcgggtc tgcgagaaga tggccctata cgacgtcacg 540
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agggttgagt acctgctcaa aatgtggcgg tcaaagaagg tgcctatggg cttttcttac 660
gacaccaggt gttttgattc aaccgtcact gagcgggaca tccggactga gaacgacatc 720
tatcagtctt gccagctgga tcccgtagca aggagggcag tatcatccct aacggaacgg 780
ctctacgtag gcggccccc atgtgaactcc aagggacagt catgtggcta ccgtagatgc 840
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gtctccgcga gcaagcttga cttatcaggc tgggttcgtgg ccggctacga cgggggggac 1680
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<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 11

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24

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 12

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34

<210> 13

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 13

tcataactctt ggaccggggc tct

23

<210> 14
<211> 24
<212> DNA
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<220>
<223> Primer

<400> 14
gtgccgctct atcgagcggg gagt

24

<210> 15
<211> 21
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<220>
<223> Primer

<400> 15
atactcctgg acagggggccc t

21

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
atactcctgg acagggggccc t

21

<210> 17
<211> 21
<212> DNA
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<220>
<223> Primer

<400> 17
ccgctctacc gagcgggggag t

21

<210> 18

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
gagcgtgggc tgctgctcta tgtc

24

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
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30

<210> 20
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<220>
<223> Primer

<400> 20
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21

<210> 21
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<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
gatcggagga cgtcgtgtgc tggt

24

<210> 22
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
gttcgatgtc atactcgtgg actg

24

<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
aagctgccta ccgagcaggc agca

24

<210> 24
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<220>
 <223> Primer

<400> 24
 ctaagctcag gctcttggtc cact

24

<210> 25
 <211> 24
 <212> DNA
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<220>
 <223> Primer

<400> 25
 gacgacgtcg tatgttggtc catg

24

<210> 26
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 26
 ctaccgagcg gggagcaaaa agatg

25

<210> 27
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> His-Tag

<400> 27
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 1 5

<210> 28
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence encoding SEQ ID NO: 27

<400> 28
ctcgagcacc accaccacca ccac

24